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*Publication date:*
2010

*Document Version*
Publisher's PDF, also known as Version of record

# The effect of different *in vitro* conditions on the metabolic footprint of *Lactobacillus acidophilus* NCFM

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*Introduction*

During the last decade, it has become evident that the complex ecosystem of microbes inhabiting the human gut plays an important role for human health. An increasing number of publications have shown that the composition and activity of our intestinal microbiota affects a number of different so-called lifestyle diseases including allergy, obesity, and colorectal cancer, as well as our susceptibility to intestinal infections and inflammation.

Additionally, it has become evident that the intestinal microbiota can be modulated by intake of pre- and probiotics. A large number of studies have addressed the effects of dietary interventions on the presence of specific bacterial metabolites, which are anticipated to play a role for gut health. However, such data evidently provide only small parts of the complex puzzle constituting the interactions between diet, microbiota, and mammalian host.

This project's objective is to elucidate the mechanism behind the beneficial effects of pre- and probiotics. This will lead to development of new pre- and probiotics targeting specific lifestyle related disorders.

*Methods*

*In vitro* fermentation tests in an anaerobic chamber were performed with *Lactobacillus acidophilus* NCFM grown under different conditions (e.g. pH, addition of prebiotics) in a semi-synthetic medium. Direct infusion mass spectrometry (MS) and liquid chromatography (LC) combined with MS is used for metabolite footprinting, performed in microTOF-Q Mass Spectrometer. Newly developed advanced ('omics-') methodologies allow analysis of biological interactions, which include statistical approach to bacterial metabolome such as principal component analysis.

*Results*

*In vitro* fermentation studies showed that pH value has a significant effect on the *Lactobacillus acidophilus* NCFM growth and metabolite footprint. Quantitative and qualitative differences in extracellular metabolite were observed by use of both direct infusion MS and LC-MS. Principal component analysis will be used for visualization of the exact metabolite variations in the samples. It is expected that later analyses will reveal specific metabolite production by *Lactobacillus acidophilus* NCFM induced by the presence of varied prebiotic carbohydrates in the semi-synthetic medium.

*Discussion*

The production of metabolites *in vitro* by *Lactobacillus acidophilus* NCFM can be affected by pH value. The same method will later on be used for studying the effect of prebiotics on the metabolite footprint. This would also allow analysis of the prebiotic candidates' beneficial potential. Future studies will include experiments in gnotobiotic mice, mono-colonized with *Lactobacillus acidophilus* NCFM. Production of specific metabolites from the bacterium and the host epithelium will be investigated as well as the metabolite profile in blood.